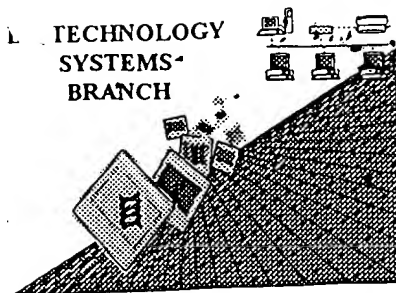


RAW SEQUENCE LISTING ERROR REPORT

TECHNOLOGY
SYSTEMS
BRANCH



2590
091

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/944 727
Source: OIPE
Date Processed by STIC: 09/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/944727

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PT

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Format Errors: Contact Robert Wax
703 308 4216
and
703 308 4119

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/944,727

DATE: 09/21/2001
TIME: 20:42:17

Input Set : A:\ES.txt
Output Set: N:\CRF3\09212001\I944727.raw

4 <110> APPLICANT: Dill Kilian
W--> 5 <120> TITLE OF INVENTION: ENZYME-AMPLIFIED REDOX MICROARRAY DETECTION
W--> 6 PROCESS
W--> 7 <130> FILE REFERENCE: 0405
W--> 8 <140> CURRENT APPLICATION NUMBER: To be assigned
9 <141> CURRENT FILING DATE: 2001-08-30
W--> 10 <160> NUMBER OF SEQ ID: 4

Does Not Comply
Corrected Diskette Needed

Errored: See Error Summary Sheet
Format Must Comply with New
CFR Rules as of July 1, 1998.

ERRORED SEQUENCES

12 <210> SEQ ID NO: 1
13 <211> LENGTH: 15
E--> 14 <212> TYPE: nucleic acid
15 <213> ORGANISM: Artificial Sequence
W--> 16 <220> FEATURE:
17 <223> OTHER INFORMATION: KRAS
W--> 18 <400> SEQUENCE: 1
20 TACGCCTCCA GCTCC 15
23 <210> SEQ ID NO: 2
24 <211> LENGTH: 15
E--> 25 <212> TYPE: nucleic acid
26 <213> ORGANISM: Artificial Sequence
W--> 27 <220> FEATURE:
28 <223> OTHER INFORMATION: rabbit fragment
W--> 29 <400> SEQUENCE: 2
31 AGGCTACGAA GACTT 15
33 <210> SEQ ID NO: 3
34 <211> LENGTH: 15
E--> 35 <212> TYPE: nucleic acid
36 <213> ORGANISM: Artificial Sequence
W--> 37 <220> FEATURE:
38 <223> OTHER INFORMATION: microarray capture probe
W--> 39 <400> SEQUENCE: 3
41 GGAGCTGGTG GCGTA 15
44 <210> SEQ ID NO: 4
45 <211> LENGTH: 18
E--> 46 <212> TYPE: nucleic acid
47 <213> ORGANISM: Artificial Sequence
W--> 48 <220> FEATURE:
49 <223> OTHER INFORMATION: microarray capture probe
W--> 50 <400> SEQUENCE: 4
52 AAGTCTTCGT CGTAGCCT 18

nucleic acid should specify
"DNA" or "RNA"

nucleotide residues must be in lower case

Errored

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

DATE: 09/21/2001

PATENT APPLICATION: US/09/944,727

TIME: 20:42:18

Input Set : A:\ES.txt

Output Set: N:\CRF3\09212001\I944727.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:283 W: Missing Blank Line separator, <140> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:283 W: Missing Blank Line separator, <160> field identifier
L:14 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:16 M:283 W: Missing Blank Line separator, <220> field identifier
L:18 M:283 W: Missing Blank Line separator, <400> field identifier
L:25 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:27 M:283 W: ~~Missing Blank Line separator, <220> field identifier~~
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:35 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:37 M:283 W: Missing Blank Line separator, <220> field identifier
L:39 M:283 W: Missing Blank Line separator, <400> field identifier
L:46 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:48 M:283 W: Missing Blank Line separator, <220> field identifier
L:50 M:283 W: Missing Blank Line separator, <400> field identifier